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10/09 OIPE  
#2

RAW SEQUENCE LISTING DATE: 06/14/2001  
PATENT APPLICATION: US/09/852,370 TIME: 11:57:01

Input Set : N:\CrF3\RULE60\09852370.txt  
Output Set: N:\CRF3\06142001\I852370.raw

3 <110> APPLICANT: Pomerantz, Joel L.  
4 Sharp, Phillip A.  
5 Pabo, Carl O.  
7 <120> TITLE OF INVENTION: Chimeric DNA-binding proteins  
9 <130> FILE REFERENCE: APV-022.02  
12 <140> CURRENT APPLICATION NUMBER: 09/852,370  
13 <141> CURRENT FILING DATE: 2001-05-10  
15 <150> PRIOR APPLICATION NUMBER: 08/973,131  
16 <151> PRIOR FILING DATE: 1997-11-26  
18 <150> PRIOR APPLICATION NUMBER: PCT/US95/16982  
19 <151> PRIOR FILING DATE: 1995-12-29  
21 <150> PRIOR APPLICATION NUMBER: 08/366,083  
22 <151> PRIOR FILING DATE: 1994-12-29  
24 <160> NUMBER OF SEQ ID NOS: 75  
26 <170> SOFTWARE: PatentIn Ver. 2.0  
28 <210> SEQ ID NO: 1  
29 <211> LENGTH: 26  
30 <212> TYPE: DNA  
31 <213> ORGANISM: Artificial Sequence  
33 <220> FEATURE:  
34 <223> OTHER INFORMATION: Description of Artificial Sequence:  
35 oligonucleotide used to determine the consensus  
36 binding sequence of ZFHD1  
38 <400> SEQUENCE: 1  
39 gtttggcacc tgactaattt aaggag  
42 <210> SEQ ID NO: 2  
43 <211> LENGTH: 25  
44 <212> TYPE: DNA  
45 <213> ORGANISM: Artificial Sequence  
47 <220> FEATURE:  
48 <223> OTHER INFORMATION: Description of Artificial Sequence:  
49 oligonucleotide used to determine the consensus  
50 binding sequence of ZFHD1  
52 <400> SEQUENCE: 2  
53 gcgttaatta agggaggtaa ggccc  
56 <210> SEQ ID NO: 3  
57 <211> LENGTH: 25  
58 <212> TYPE: DNA  
59 <213> ORGANISM: Artificial Sequence  
61 <220> FEATURE:  
62 <223> OTHER INFORMATION: Description of Artificial Sequence:  
63 oligonucleotide used to determine the consensus  
64 binding sequence of ZFHD1  
66 <400> SEQUENCE: 3  
67 ctccggccgtt aatgaggagggt gttcg  
70 <210> SEQ ID NO: 4  
71 <211> LENGTH: 25

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72 <212> TYPE: DNA  
 73 <213> ORGANISM: Artificial Sequence  
 75 <220> FEATURE:  
 76 <223> OTHER INFORMATION: Description of Artificial Sequence:  
 77 oligonucleotide used to determine the consensus  
 78 binding sequence of ZFHD1  
 80 <400> SEQUENCE: 4  
 81 taattatggg cgggatcgaa tagcc 25  
 84 <210> SEQ ID NO: 5  
 85 <211> LENGTH: 26  
 86 <212> TYPE: DNA  
 87 <213> ORGANISM: Artificial Sequence  
 89 <220> FEATURE:  
 90 <223> OTHER INFORMATION: Description of Artificial Sequence:  
 91 oligonucleotide used to determine the consensus  
 92 binding sequence of ZFHD1  
 94 <400> SEQUENCE: 5  
 95 ggcataatac aatcctttaa ttatgg 26  
 98 <210> SEQ ID NO: 6  
 99 <211> LENGTH: 26  
 100 <212> TYPE: DNA  
 101 <213> ORGANISM: Artificial Sequence  
 103 <220> FEATURE:  
 104 <223> OTHER INFORMATION: Description of Artificial Sequence:  
 105 oligonucleotide used to determine the consensus  
 106 binding sequence of ZFHD1  
 108 <400> SEQUENCE: 6  
 109 ggccgtacct catgaaatata gggcgcg 26  
 112 <210> SEQ ID NO: 7  
 113 <211> LENGTH: 25  
 114 <212> TYPE: DNA  
 115 <213> ORGANISM: Artificial Sequence  
 117 <220> FEATURE:  
 118 <223> OTHER INFORMATION: Description of Artificial Sequence:  
 119 oligonucleotide used to determine the consensus  
 120 binding sequence of ZFHD1  
 122 <400> SEQUENCE: 7  
 123 gttaattatg gggtaataat ggtgc 25  
 126 <210> SEQ ID NO: 8  
 127 <211> LENGTH: 25  
 128 <212> TYPE: DNA  
 129 <213> ORGANISM: Artificial Sequence  
 131 <220> FEATURE:  
 132 <223> OTHER INFORMATION: Description of Artificial Sequence:  
 133 oligonucleotide used to determine the consensus  
 134 binding sequence of ZFHD1  
 136 <400> SEQUENCE: 8  
 137 gtcgggctct gttaattatg ggtgg 25  
 140 <210> SEQ ID NO: 9

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Input Set : N:\Crf3\RULE60\09852370.txt  
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141 <211> LENGTH: 25  
142 <212> TYPE: DNA  
143 <213> ORGANISM: Artificial Sequence  
145 <220> FEATURE:  
146 <223> OTHER INFORMATION: Description of Artificial Sequence:  
147 oligonucleotide used to determine the consensus  
148 binding sequence of ZFHD1  
150 <400> SEQUENCE: 9  
151 ggataattac gggttggcatt taggc 25  
154 <210> SEQ ID NO: 10  
155 <211> LENGTH: 25  
156 <212> TYPE: DNA  
157 <213> ORGANISM: Artificial Sequence  
159 <220> FEATURE:  
160 <223> OTHER INFORMATION: Description of Artificial Sequence:  
161 oligonucleotide used to determine the consensus  
162 binding sequence of ZFHD1  
164 <400> SEQUENCE: 10  
165 gataaatagg ggcgtcccat cccgt 25  
168 <210> SEQ ID NO: 11  
169 <211> LENGTH: 24  
170 <212> TYPE: DNA  
171 <213> ORGANISM: Artificial Sequence  
173 <220> FEATURE:  
174 <223> OTHER INFORMATION: Description of Artificial Sequence:  
175 oligonucleotide used to determine the consensus  
176 binding sequence of ZFHD1  
178 <400> SEQUENCE: 11  
179 taaatttaggg cttaattac ggtc 24  
182 <210> SEQ ID NO: 12  
183 <211> LENGTH: 25  
184 <212> TYPE: DNA  
185 <213> ORGANISM: Artificial Sequence  
187 <220> FEATURE:  
188 <223> OTHER INFORMATION: Description of Artificial Sequence:  
189 oligonucleotide used to determine the consensus  
190 binding sequence of ZFHD1  
192 <400> SEQUENCE: 12  
193 tcatttagt gttaatgaga tgcgc 25  
196 <210> SEQ ID NO: 13  
197 <211> LENGTH: 26  
198 <212> TYPE: DNA  
199 <213> ORGANISM: Artificial Sequence  
201 <220> FEATURE:  
202 <223> OTHER INFORMATION: Description of Artificial Sequence:  
203 oligonucleotide used to determine the consensus  
204 binding sequence of ZFHD1  
206 <400> SEQUENCE: 13  
207 tagttgctaa tttgtattaa ttaaag 26

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Input Set : N:\Crf3\RULE60\09852370.txt  
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210 <210> SEQ ID NO: 14  
211 <211> LENGTH: 25  
212 <212> TYPE: DNA  
213 <213> ORGANISM: Artificial Sequence  
215 <220> FEATURE:  
216 <223> OTHER INFORMATION: Description of Artificial Sequence:  
217 oligonucleotide used to determine the consensus  
218 binding sequence of ZFHD1  
220 <400> SEQUENCE: 14 25  
221 agttatataat taagaatgtt aatta  
224 <210> SEQ ID NO: 15  
225 <211> LENGTH: 25  
226 <212> TYPE: DNA  
227 <213> ORGANISM: Artificial Sequence  
229 <220> FEATURE:  
230 <223> OTHER INFORMATION: Description of Artificial Sequence:  
231 oligonucleotide used to determine the consensus  
232 binding sequence of ZFHD1  
234 <400> SEQUENCE: 15 25  
235 gtgtgataat gagctggtcc gtccc  
238 <210> SEQ ID NO: 16  
239 <211> LENGTH: 25  
240 <212> TYPE: DNA  
241 <213> ORGANISM: Artificial Sequence  
243 <220> FEATURE:  
244 <223> OTHER INFORMATION: Description of Artificial Sequence:  
245 oligonucleotide used to determine the consensus  
246 binding sequence of ZFHD1  
248 <400> SEQUENCE: 16 25  
249 atattaaggc gtaattcggga caaga  
252 <210> SEQ ID NO: 17  
253 <211> LENGTH: 12  
254 <212> TYPE: DNA  
255 <213> ORGANISM: Artificial Sequence  
257 <220> FEATURE:  
258 <223> OTHER INFORMATION: Description of Artificial Sequence: consensus  
259 binding sequence of ZFHD1  
261 <220> FEATURE:  
262 <223> OTHER INFORMATION: "n" represents a, t, c, g or other  
264 <400> SEQUENCE: 17 12  
W--> 265 taattanggg ng  
268 <210> SEQ ID NO: 18  
269 <211> LENGTH: 12  
270 <212> TYPE: DNA  
271 <213> ORGANISM: Artificial Sequence  
273 <220> FEATURE:  
274 <223> OTHER INFORMATION: Description of Artificial Sequence: hybrid DNA  
275 site  
277 <220> FEATURE:

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Input Set : N:\Crf3\RULE60\09852370.txt  
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278 <223> OTHER INFORMATION: "n" represents a, t, c, g or other  
280 <400> SEQUENCE: 18  
W--> 281 aaatnntggg cg 12  
284 <210> SEQ ID NO: 19  
285 <211> LENGTH: 12  
286 <212> TYPE: DNA  
287 <213> ORGANISM: Artificial Sequence  
289 <220> FEATURE:  
290 <223> OTHER INFORMATION: Description of Artificial Sequence: predicted  
291 binding sequence  
293 <220> FEATURE:  
294 <223> OTHER INFORMATION: "n" represents a, t, c, g or other  
296 <400> SEQUENCE: 19  
W--> 297 cgccccanaaa at 12  
300 <210> SEQ ID NO: 20  
301 <211> LENGTH: 10  
302 <212> TYPE: DNA  
303 <213> ORGANISM: human  
305 <400> SEQUENCE: 20  
306 atgcaaatga 10  
309 <210> SEQ ID NO: 21  
310 <211> LENGTH: 12  
311 <212> TYPE: DNA  
312 <213> ORGANISM: Artificial Sequence  
314 <220> FEATURE:  
315 <223> OTHER INFORMATION: Description of Artificial Sequence: hybrid binding  
316 site  
318 <400> SEQUENCE: 21  
319 taatgatggg cg 12  
322 <210> SEQ ID NO: 22  
323 <211> LENGTH: 63  
324 <212> TYPE: DNA  
325 <213> ORGANISM: Artificial Sequence  
327 <220> FEATURE:  
328 <223> OTHER INFORMATION: Description of Artificial Sequence: hybid binding  
329 site  
331 <220> FEATURE:  
332 <223> OTHER INFORMATION: "n" represents a, t, c, g or other  
334 <400> SEQUENCE: 22  
W--> 335 ggctgagtct gaacggatcc nnnnnnnnnn nnnnnnnnnn nnnnnccctcg agactgagcg 60  
337 tcg 63  
340 <210> SEQ ID NO: 23  
341 <211> LENGTH: 12  
342 <212> TYPE: DNA  
343 <213> ORGANISM: Artificial Sequence  
345 <220> FEATURE:  
346 <223> OTHER INFORMATION: Description of Artificial Sequence: probe  
348 <400> SEQUENCE: 23  
349 tcattatggg cg 12

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/852,370

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Input Set : N:\Crf3\RULE60\09852370.txt  
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L:265 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:17  
L:265 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17  
L:265 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:281 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:18  
L:281 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:18  
L:281 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:297 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:19  
L:297 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:19  
L:297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19  
L:335 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:22  
L:335 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22  
L:335 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:657 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:657 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:841 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:841 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:869 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:869 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:908 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:908 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: